



Copy

Applicant's Copy

Application No.: 09/357,675

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- 7. Other: \_\_\_\_\_

**Applicant Must Provide:**

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

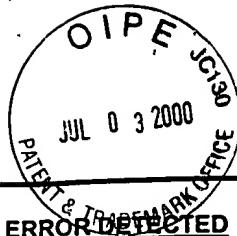
For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**



## Raw Sequence Listing Error Summary

### ERROR DETECTED   SUGGESTED CORRECTION

SERIAL NUMBER: 09/357,675

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleic  
The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2  Wrapped Aminos  
The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3  Incorrect Line Length  
The rules require that a line not exceed 72 characters in length. This includes spaces.

4  Misaligned Amino Acid Numbering  
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5  Non-ASCII  
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6  Variable Length  
Sequence(s)  contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7  PatentIn ver. 2.0 "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)  . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8  Skipped Sequences (OLD RULES)  
Sequence(s)  missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9  Skipped Sequences (NEW RULES)  
Sequence(s)  missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

10  Use of n's or Xaa's (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which n  
SEQ ID NOS: 1,4,5  
Use of "n's"

11  Use of <213>Organism (NEW RULES)  
Sequence(s)  are missing this mandatory field or its response.

12  Use of <220>Feature (NEW RULES)  
Sequence(s)  are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or UNKNOWN.  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13  PatentIn ver. 2.0 "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

Shukla



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1632

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/357,675

DATE: 11/09/1999  
TIME: 11:27:24

Input Set: I357675.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Croce M.D., Carlo M.  
2 <120> TITLE OF INVENTION: Nitrilase Homologs  
3 <130> FILE REFERENCE: CRO01 NP001 Nitrilase Homologs  
4 <140> CURRENT APPLICATION NUMBER: US/09/357,675  
5 <141> CURRENT FILING DATE: 1999-07-20  
6 <150> EARLIER APPLICATION NUMBER: 60/093,350  
7 <151> EARLIER FILING DATE: 1998-07-20  
8 <160> NUMBER OF SEQ ID NOS: 18  
9 <170> SOFTWARE: PatentIn Ver. 2.1  
10 <210> SEQ ID NO 1  
11 <211> LENGTH: 1416  
12 <212> TYPE: DNA  
13 <213> ORGANISM: Homo sapiens  
14 <400> SEQUENCE: 1  
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16 ttttggctat atcttcattt aggacactact ccctatcccg tcggccgcgg ctgggcttca 120  
17 tcaccaggcc tcctcacaga ttccctgtccc ttctgtgtcc tggactccgg atacctcaac 180  
18 tctcagtaact ttgtgctcaag cccaggccca gagccatggc tatctcctct tcctcctgcg 240  
19 aactggccctt ggtggctgtg tgccaggtaa catcgacgccc agacaagcaa cagaacttta 300  
20 aaacatgtgc tgagctgggtt cgagaggctg ccagactggg tgccctgcctg gctttccctgc 360  
21 ctgaggcatt tgacttcattt gcacggacc ctgcagagac gctacacccctg tctgaaccac 420  
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23 ccttgggtgg tttccatgag cgtggccaag actgggagca gactcagaaa atctacaattt 540  
24 gtcacgtgct gctgaacagc aaaggggcag tagtggccac ttacaggaag acacatctgt 600  
25 gtgacgtaga gattccagggg cagggccctt tttgtgaaag caactctacc atgcctggc 660  
26 ccagtcttgc gtcacctgtc agcacaccag caggcaagat tggcttagct gtctgctatg 720  
27 acatgcgggtt ccctgaactc tctctggcat tggctcaagc tggagcagag atacttaccc 780  
28 atccttcagc ttttggatcc attacaggcc cagcccactg ggaggtgtt ctgcggggccc 840  
29 gtgctatcga aacccagtgc tatgttagtgg cagcagcaca gtgtggacgc caccatgaga 900  
30 agagagcaag ttatggccac agcatggtgg tagaccctg gggAACAGTG gtggcccgct 960  
31 gctctgaggg gccaggcctc tgccttgcgg gaatagaccc caactatctg cgacagtgc 1020  
32 gcccacacctt gcctgtgttc cagcacccgc ggcctgaccc ctatggcaat ctgggtcacc 1080  
33 cactgtctta agacttgact tctgtgagtt tagacctgccc cctcccccaccc ccaccctgccc 1140  
34 actatgagct agtgcctatg tgacttggag gcaggatccca ggcacagctc ccctcacttg 1200  
35 gagaaccttg actcttgc tggAACACAG atgggctgtct tggggaaagaa actttcacct 1260  
36 gagcttcacc tgaggtcaga ctgcagtttcc agaaagggtgg aatttttatat agtcattgtt 1320  
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38 taatcataaa gtcaaaaaaaaaaaaaaa aaaaaaaaaa 1416  
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40 <211> LENGTH: 23  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Homo sapiens  
43 <400> SEQUENCE: 2  
44 tctgaaactg cagtctgacc tca

Does Not Comply  
Corrected Diskette Needed

see p. 2, 100

see item 10 on Env Summary Sheet

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/357,675DATE: 11/09/1999  
TIME: 11:27:24

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 47 <212> TYPE: DNA  
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 53 <212> TYPE: DNA  
 54 <213> ORGANISM: Homo sapiens  
 55 <400> SEQUENCE: 4 *idem 10*  
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 58 <211> LENGTH: 26  
 59 <212> TYPE: DNA  
 60 <213> ORGANISM: Homo sapiens *idem 10*  
 61 <400> SEQUENCE: 5  
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 64 <211> LENGTH: 21  
 65 <212> TYPE: DNA  
 66 <213> ORGANISM: Drosophila melanogaster  
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 76 <211> LENGTH: 20  
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 78 <213> ORGANISM: Caenorhabditis elegans  
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 88 <211> LENGTH: 19  
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 91 <400> SEQUENCE: 10  
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 93 <210> SEQ ID NO 11  
 94 <211> LENGTH: 20

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/357,675DATE: 11/09/1999  
TIME: 11:27:24

Input Set: I357675.RAW

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96 <213> ORGANISM: Homo sapiens  
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99 <210> SEQ ID NO 12  
100 <211> LENGTH: 21  
101 <212> TYPE: DNA  
102 <213> ORGANISM: Homo sapiens  
103 <400> SEQUENCE: 12  
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105 <210> SEQ ID NO 13  
106 <211> LENGTH: 24  
107 <212> TYPE: DNA  
108 <213> ORGANISM: Homo sapiens  
109 <400> SEQUENCE: 13  
110 aaactgaagc ctctttcctc tgac 24  
111 <210> SEQ ID NO 14  
112 <211> LENGTH: 20  
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130 <211> LENGTH: 36  
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132 <213> ORGANISM: Homo sapiens  
133 <400> SEQUENCE: 17  
134 tgacgtcgac atatgtcaac tctagttat accacg 36  
135 <210> SEQ ID NO 18  
136 <211> LENGTH: 25  
137 <212> TYPE: DNA  
138 <213> ORGANISM: Homo sapiens  
139 <400> SEQUENCE: 18  
140 tgggtacctc gactagctta tgtcc 25

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VERIFICATION SUMMARY  
PATENT APPLICATION US/09/357,675

DATE: 11/09/1999  
TIME: 11:27:24

Input Set: I357675.RAW

Line ? Error/Warning	Original Text
15 W "N" or "Xaa" used: Feature required	gcccactcgc tgcggcctnt ctggctccag accgcct
56 W "N" or "Xaa" used: Feature required	gtngtnccng gncaygtngt
62 W "N" or "Xaa" used: Feature required	acrtgnacrt gytnacngt ytgnge